SEQUENCE LISTING

<110> Daniel Cohen
      Ilya Chumakov

<120> TREATMENT OF CNS DISORDERS USING D-AMINO ACID OXIDASE AND D-ASPARTATE
      OXIDASE ANTAGONISTS

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21

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31

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acc acc acc gac gtg gct gcc ggc ctc tgg cag ccc tac ctt tct gac      317
Thr Thr Thr Asp Val Ala Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp
            45                      50                      55

ccc aac aac cca cag gag gcg gac tgg agc caa cag acc ttt gac tat      365
Pro Asn Asn Pro Gln Glu Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr
        60                      65                      70

ctc ctg agc cat gtc cat tct ccc aac gct gaa aac ctc ggc ctg ttc      413
Leu Leu Ser His Val His Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe
75                      80                      85                  90

cta atc tcg ggc tac aac ctc ttc cat gaa gcc att ccg gac cct tcc      461
Leu Ile Ser Gly Tyr Asn Leu Phe His Glu Ala Ile Pro Asp Pro Ser
                95                      100                     105

tgg aag gac aca gtt ctg gga ttt cgg aag ctg acc ccc aga gag ctg      509
Trp Lys Asp Thr Val Leu Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu
                    110                     115                     120

gat atg ttc cca gat tac ggc tat ggc tgg ttc cac aca agc cta att      557
Asp Met Phe Pro Asp Tyr Gly Tyr Gly Trp Phe His Thr Ser Leu Ile
            125                     130                     135

ctg gag gga aag aac tat cta cag tgg ctg act gaa agg tta act gag      605
Leu Glu Gly Lys Asn Tyr Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu
        140                     145                     150

agg gga gtg aag ttc ttc cag cgg aaa gtg gag tct ttt gag gag gtg      653
Arg Gly Val Lys Phe Phe Gln Arg Lys Val Glu Ser Phe Glu Glu Val
155                     160                     165                 170

gca aga gaa ggc gca gac gtg att gtc aac tgc act ggg gta tgg gct      701
Ala Arg Glu Gly Ala Asp Val Ile Val Asn Cys Thr Gly Val Trp Ala
                175                     180                     185

ggg gcg cta caa cga gac ccc ctg ctg cag cca ggc cgg ggg cag atc      749
Gly Ala Leu Gln Arg Asp Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile
                190                     195                     200

atg aag gtg gac gcc cct tgg atg aag cac ttc att ctc acc cat gac      797
Met Lys Val Asp Ala Pro Trp Met Lys His Phe Ile Leu Thr His Asp
                205                     210                     215

cca gag aga ggc atc tac aat tcc ccg tac atc atc cca ggg acc cag      845
Pro Glu Arg Gly Ile Tyr Asn Ser Pro Tyr Ile Ile Pro Gly Thr Gln
        220                     225                     230

aca gtt act ctt gga ggc atc ttc cag ttg gga aac tgg agt gaa cta      893
Thr Val Thr Leu Gly Gly Ile Phe Gln Leu Gly Asn Trp Ser Glu Leu
235                     240                     245                 250

aac aat atc cag gac cac aac acc att tgg gaa ggc tgc tgc aga ctg      941
Asn Asn Ile Gln Asp His Asn Thr Ile Trp Glu Gly Cys Cys Arg Leu
                255                     260                     265

gag ccc aca ctg aag aat gca aga att att ggt gaa cga act ggc ttc      989
Glu Pro Thr Leu Lys Asn Ala Arg Ile Ile Gly Glu Arg Thr Gly Phe
                270                     275                     280

cgg cca gta cgc ccc cag att cgg cta gaa aga gaa cag ctt cgc act     1037
Arg Pro Val Arg Pro Gln Ile Arg Leu Glu Arg Glu Gln Leu Arg Thr
            285                     290                     295

gga cct tca aac aca gag gtc atc cac aac tat ggc cat gga ggc tac     1085
Gly Pro Ser Asn Thr Glu Val Ile His Asn Tyr Gly His Gly Gly Tyr
        300                     305                     310

ggg ctc acc atc cac tgg gga tgt gcc ctg gag gca gcc aag ctc ttt     1133
Gly Leu Thr Ile His Trp Gly Cys Ala Leu Glu Ala Ala Lys Leu Phe
315                     320                     325                 330

ggg aga atc ctg gaa gaa aag aaa ttg tcc aga atg cca cca tcc cac     1181
Gly Arg Ile Leu Glu Glu Lys Lys Leu Ser Arg Met Pro Pro Ser His
                335                     340                     345

ctc tga agactccagt gactgctgcc tcccccaca agaactccct tctccctca     1237
Leu  *
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gccaatgaat caatgtgctc cttcataagc cattgcttct ccctcacttc tttcctcaaa      1297
gaagcatgag gtgagagaaa gccacaaagt cagtgcctgg agaagggttc agcccaacat      1357
ggggcccctc tcatcactga aatccctcta ccttctctgg gtctggcatt ataaagaaca      1417
gctgaggctg tcattccatg agtcttcaga agaaaggaca gctcagaaaa tcaaagaggc      1477
caactgccca gagccacaga aaatggagga taattgaggc taagtaacct gattacaagt      1537
tgtactaaca tattaaaggt tctgaaaagt cctgcagcaa agacaactat ctgatgttgt      1597
ttaacccagt gcttgctaaa cctatctggc tatggaactc ttttgcccag agcacccatg      1657
aatgccatga cacaaatctg agaaaatgct ggaa                                  1691


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tcctccatgt tattcacagg gtctcagcac gattcatctc aaagcagcga aacaagcact       120
ggcctcagaa gaagcaatat taaaacagtt acaactcatc tagcgcacag acacccaact       180
gacaccctgt tcctccagtc ataacaacaa ctacagcttt gattgaacaa gagactgagt       240
ttggtaactt tctcctaata aaaagatcac tgactatgga ctgcttctgg tggggttacg       300
aaaccgcaac ctcatgtgcc tgcatttcct gaaaagacat tttgatgtag gaagggcctg       360
gagtcctgct gcttgcgtct ctgggatacg ggagcaaaga gccacgcatc ctcatggccc       420
acacaggcgt cacctccagt ctctccttgg cctcatctcc ccagcgtcct ggaatggcat       480
cgggctggcc cagggagccc ctgtcctgtg cctctccttt ccctcaggg gctgcaggcc        540
tgaccacccc caccgcaggc caggcctaca gtgccccatg gaacgtcctg accctccccc      600
agggtggcag caggaagaag gaagaaaggg gatcctctcc agctggcag agagacagac       660
cttcttgtgc tcatcaaccc tccaagaatg cctgccctcc ctccttcccc caaggcctgt      720
ccacagggc ttgagatcag ccagaaactt caggcaactt ttcagggact gggagcgagg       780
tctcccggcc gggcctgggt ccagtctctg tgggcagtgc agtgccgagc cccaccctc        840
aagccgtgcc ctgtccatag ctccagactt tgaccctgca ctccagtccg ggctggcgga       900
cagagggctg gaaacaagac gctccagaat caggagcttc ccctcaggaa atagcatcct       960
gtgtcccgc actgcagttg tctggtctct ccagcagttt ggtacttccg atgaagagct      1020
tgtgtctcca gaggcaaagt atggggaag agggaagaga gccagaccaag ggtccctgag      1080
aggggctgtc ccctaagccc cagtatccaa gctcgggctc gaagctggaa ggagaattgc      1140
ctagaggctg ctcgca atg cgt gtg gtg gtg att gga gca gga gtc atc ggg      1191
                     Met Arg Val Val Val Ile Gly Ala Gly Val Ile Gly
                      1               5                  10
ctg tcc acc gcc ctc tgc atc cat gag cgc tac cac tca gtc ctg cag      1239
Leu Ser Thr Ala Leu Cys Ile His Glu Arg Tyr His Ser Val Leu Gln
         15                  20                  25
cca ctg gac ata aag gtc tac gcg gac cgc ttc acc cca ctc acc acc      1287
Pro Leu Asp Ile Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr
     30                  35                  40
acc gac gtg gct gcc ggc ctc tgg cag ccc tac ctt tct gac ccc aac      1335
Thr Asp Val Ala Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn
 45                  50                  55                  60
aac cca cag gag gcg gac tgg agc caa cag acc ttt gac tat ctc ctg      1383
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33

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Asn Pro Gln Glu Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu
            65                  70                  75
agc cat gtc cat tct ccc aac gct gaa aac ctg ggc ctg ttc cta atc      1431
Ser His Val His Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile
        80                  85                  90
tcg ggc tac aac ctc ttc cat gaa gcc att ccg gac cct tcc tgg aag      1479
Ser Gly Tyr Asn Leu Phe His Glu Ala Ile Pro Asp Pro Ser Trp Lys
            95                 100                 105
gac aca gtt ctg gga ttt cgg aag ctg acc ccc aga gag ctg gat atg      1527
Asp Thr Val Leu Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu Asp Met
        110                 115                 120
ttc cca gat tac ggc tat ggc tgg ttc cac aca agc cta att ctg gag      1575
Phe Pro Asp Tyr Gly Tyr Gly Trp Phe His Thr Ser Leu Ile Leu Glu
    125                 130                 135                 140
gga aag aac tat cta cag tgg ctg act gaa agg tta act gag agg gga      1623
Gly Lys Asn Tyr Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu Arg Gly
                145                 150                 155
gtg aag ttc ttc cag cgg aaa gtg gag tct ttt gag gag gtg gca aga      1671
Val Lys Phe Phe Gln Arg Lys Val Glu Ser Phe Glu Glu Val Ala Arg
            160                 165                 170
gaa ggc gca gac gtg att gtc aac tgc act ggg gta tgg gct ggg gcg      1719
Glu Gly Ala Asp Val Ile Val Asn Cys Thr Gly Val Trp Ala Gly Ala
        175                 180                 185
cta caa cga gac ccc ctg ctg cag cca ggc cgg ggg cag atc atg aag      1767
Leu Gln Arg Asp Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile Met Lys
        190                 195                 200
gac cca gac agt tac tct tgg agg cat ctt cca gtt ggg aaa ctg gag      1815
Asp Pro Asp Ser Tyr Ser Trp Arg His Leu Pro Val Gly Lys Leu Glu
    205                 210                 215                 220
tga actaaacaat atccaggacc acaacaccat ttgggaaggc tgctgcagac           1868
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tggagcccac actgaagaat gcaagaatta ttggtgaacg aactggcttc cggccagtac   1928
gcccccagat tcggctagaa agagaacagc ttcgcactgg accttcaaac acagaggtca   1988
tccacaacta tggccatgga ggctacgggc tcaccatcca ctggggatgt gccctggagg   2048
cagccaagct ctttgggaga atcctggaag aaaagaaatt gtccagaatg ccaccatccc   2108
acctctgaag actccagtga ctgctgcctc cccccacaag aactcccttc tccctcagc    2168
caatgaatca atgtgctcct tcataagcca ttgcttcctc ctcacttctt tcctcaaaga   2228
agcatgaggt gagagaaagc cacaaagtca gtgcctggag aagggtcag cccaacatgg    2288
ggcccctctc atcactgaaa tccctctacc ttctctgggt ctggcattat aaagaacagc   2348
tgaggctgtc attccatgag tcttcagaag aaaggacagc tcagaaaatc aaagaggcca   2408
actgcccaga gccacagaaa atggaggata attgaggcta agtaacctga ttacaagttg   2468
tactaacata ttaaaggttc tgaaaagtcc tgcagcaaag acaactatct gatgttgttt   2528
aacccagtgc ttgctaaacc tatctggcta tggaactctt ttgcccagag cacccatgaa   2588
tgccatgaca caaatctgag aaaatgctgg aa                                 2620


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cttcccctca ggaaatagca tcctgtgtcc ccgcactgca gttgtctggt ctctccagca   120
gtttggtact tccggctgct gca atg cgt gtg gtg gtg att gga gca gga gtc   173
                         Met Arg Val Val Val Ile Gly Ala Gly Val
                          1   5   10
atc ggg ctg tcc acc gcc ctc tgc atc cat gag cgc tac cac tca gtc   221
Ile Gly Leu Ser Thr Ala Leu Cys Ile His Glu Arg Tyr His Ser Val
               15   20   25
ctg cag cca ctg gac ata aag gtc tac gcg gac cgc ttc acc cca ctc   269
Leu Gln Pro Leu Asp Ile Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu
           30   35   40
acc acc acc gac gtg gct gcc ggc ctc tgg cag ccc tac ctt tct gac   317
Thr Thr Thr Asp Val Ala Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp
       45   50   55
ccc aac aac cca cag gag gcg acc ctt cct gga agg aca cag ttc tgg   365
Pro Asn Asn Pro Gln Glu Ala Thr Leu Pro Gly Arg Thr Gln Phe Trp
   60   65   70
gat ttc gga agc tga cccccagaga gctggatatg ttcccagatt acggctatgg   420
Asp Phe Gly Ser *
75
ctggttccac acaagcctaa ttctggaggg aaagaactat ctacagtggc tgactgaaag   480
gttaactgag aggggagtga agttcttcca gcggaaagtg gagtcttttg aggaggtggc   540
aagagaaggc gcagacgtga ttgtcaactg cactggggta tgggctgggg cgctacaacg   600
agaccccctg ctgcagccag gccggggggca gatcatgaag gtggacgccc cttggatgaa   660
gcacttcatt ctcacccatg acccagagag aggcatctac aattccccgt acatcatccc   720
agggacccag acagttactc ttggaggcat cttccagttg ggaaactgga gtgaactaaa   780
caatatccag gaccacaaca ccatttggga aggctgctgc agactggagc ccacactgaa   840
gaatgcaaga attattggtg aacgaactgg cttccggcca gtacgccccc agattcggct   900
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gaaaatggag gataattgag gctaagtaac ctgattacaa gttgtactaa catattaaag 1440
gttctgaaaa gtcctgcagc aaagacaact atctgatgtt gtttaaccca gtgcttgcta 1500
aacctatctg gctatggaac tcttttgccc agagcaccca tgaatgccat gacacaaatc 1560
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tcctccatgt tattcacagg gtctcagcac gattcatctc aaaggctgct gca atg        116
                                                              Met
                                                                1

cgt gtg gtg gtg att gga gca gga gtc atc ggg ctg tcc acc gcc ctc       164
Arg Val Val Val Ile Gly Ala Gly Val Ile Gly Leu Ser Thr Ala Leu
            5                   10                  15

tgc atc cat gag cgc tac cac tca gtc ctg cag cca ctg gac ata aag       212
Cys Ile His Glu Arg Tyr His Ser Val Leu Gln Pro Leu Asp Ile Lys
        20                  25                  30

gtc tac gcg gac cgc ttc acc cca ctc acc acc acc gac gtg gct gcc       260
Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala Ala
    35                  40                  45

ggc ctc tgg cag ccc tac ctt tct gac ccc aac aac cca cag gag gcg       308
Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu Ala
50                  55                  60                  65

gac tgg agc caa cag acc ttt gac tat ctc ctg agc cat gtc cat tct       356
Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu Ser His Val His Ser
                70                  75                  80

ccc aac gct gaa aac ctg ggc ctg ttc cta atc tcg ggc tac aac ctc       404
Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile Ser Gly Tyr Asn Leu
            85                  90                  95

ttc cat gaa gcc att ccg gtg gca aga gaa ggc gca gac gtg att gtc       452
Phe His Glu Ala Ile Pro Val Ala Arg Glu Gly Ala Asp Val Ile Val
            100                 105                 110

aac tgc act ggg gta tgg gct ggg gcg cta caa cga gac ccc ctg ctg       500
Asn Cys Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp Pro Leu Leu
        115                 120                 125

cag cca ggc cgg ggg cag atc atg aag gtg gac gcc cct tgg atg aag       548
Gln Pro Gly Arg Gly Gln Ile Met Lys Val Asp Ala Pro Trp Met Lys
130                 135                 140                 145

cac ttc att ctc acc cat gac cca gag agg ggc atc tac aat tcc ccg       596
His Phe Ile Leu Thr His Asp Pro Glu Arg Gly Ile Tyr Asn Ser Pro
                150                 155                 160

tac atc atc cca ggg acc cag aca gtt act ctt gga ggc atc ttc cag       644
Tyr Ile Ile Pro Gly Thr Gln Thr Val Thr Leu Gly Gly Ile Phe Gln
            165                 170                 175

ttg gga aac tgg agt gaa cta aac aat atc cag gac cac aac acc att       692
Leu Gly Asn Trp Ser Glu Leu Asn Asn Ile Gln Asp His Asn Thr Ile
            180                 185                 190

tgg gaa ggc tgc tgc aga ctg gag ccc aca ctg aag aat gca aga att       740
Trp Glu Gly Cys Cys Arg Leu Glu Pro Thr Leu Lys Asn Ala Arg Ile
        195                 200                 205

att ggt gaa cga act ggc ttc cgg cca gta cgc ccc cag att cgg cta       788
Ile Gly Glu Arg Thr Gly Phe Arg Pro Val Arg Pro Gln Ile Arg Leu
210                 215                 220                 225

gaa aga gaa cag ctt cgc act gga cct tca aac aca gag gtc atc cac       836
Glu Arg Glu Gln Leu Arg Thr Gly Pro Ser Asn Thr Glu Val Ile His
                230                 235                 240

aac tat ggc cat gga ggc tac ggg ctc acc atc cac tgg gga tgt gcc       884
Asn Tyr Gly His Gly Gly Tyr Gly Leu Thr Ile His Trp Gly Cys Ala
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36

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                245                      250                      255
ctg gag gca gcc aag ctc ttt ggg aga atc ctg gaa gaa aag aaa ttg        932
Leu Glu Ala Ala Lys Leu Phe Gly Arg Ile Leu Glu Glu Lys Lys Leu
        260                      265                      270
tcc aga atg cca cca tcc cac ctc tga agactccagt gactgctgcc              979
Ser Arg Met Pro Pro Ser His Leu  *
    275                      280
tccccccaca agaactccct tctcccctca gccaatgaat caatgtgctc cttcataagc      1039
cattgcttct ccctcacttc tttcctcaaa gaagcatgag gtgagagaaa gccacaaagt      1099
cagtgcctgg agaagggttc agcccaacat gggcgccctc tcatcactga aatccctcta      1159
ccttctctgg gtctggcatt ataaagaaca gctgaggctg tcattccatg agtcttcaga      1219
agaaaggaca gctcagaaaa tcaaagaggc caactgccca gagccacaga aaatgggaga      1279
taattgaggc taagtaacct gattacaagt tgtactaaca tattaaaggt tctgaaaagt      1339
cctgca                                                                 1345


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<213> Homo sapiens

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Met Arg Val Val Val Ile Gly Ala Gly Val Ile Gly Leu Ser Thr Ala
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Leu Cys Ile His Glu Arg Tyr His Ser Val Leu Gln Pro Leu Asp Ile
            20                  25                  30
Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala
        35                  40                  45
Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu
    50                  55                  60
Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu Ser His Val His
65                  70                  75                  80
Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile Ser Gly Tyr Asn
                85                  90                  95
Leu Phe His Glu Ala Ile Pro Asp Pro Ser Trp Lys Asp Thr Val Leu
            100                 105                 110
Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu Asp Met Phe Pro Asp Tyr
        115                 120                 125
Gly Tyr Gly Trp Phe His Thr Ser Leu Ile Leu Glu Gly Lys Asn Tyr
    130                 135                 140
Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu Arg Gly Val Lys Phe Phe
145                 150                 155                 160
Gln Arg Lys Val Glu Ser Phe Glu Glu Val Ala Arg Glu Gly Ala Asp
                165                 170                 175
Val Ile Val Asn Cys Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp
            180                 185                 190
Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile Met Lys Val Asp Ala Pro
        195                 200                 205
Trp Met Lys His Phe Ile Leu Thr His Asp Pro Glu Arg Gly Ile Tyr
    210                 215                 220
Asn Ser Pro Tyr Ile Ile Pro Gly Thr Gln Thr Val Thr Leu Gly Gly
225                 230                 235                 240
Ile Phe Gln Leu Gly Asn Trp Ser Glu Leu Asn Asn Ile Gln Asp His
                245                 250                 255
Asn Thr Ile Trp Glu Gly Cys Cys Arg Leu Glu Pro Thr Leu Lys Asn
            260                 265                 270
Ala Arg Ile Ile Gly Glu Arg Thr Gly Phe Arg Pro Val Arg Pro Gln
        275                 280                 285
Ile Arg Leu Glu Arg Glu Gln Leu Arg Thr Gly Pro Ser Asn Thr Glu
    290                 295                 300
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Val Ile His Asn Tyr Gly His Gly Gly Tyr Gly Leu Thr Ile His Trp
305                 310                 315                 320
Gly Cys Ala Leu Glu Ala Ala Lys Leu Phe Gly Arg Ile Leu Glu Glu
                325                 330                 335
Lys Lys Leu Ser Arg Met Pro Pro Ser His Leu
            340                 345
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<210> 8
<211> 220
<212> PRT
<213> Homo sapiens

<400> 8
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1               5                   10                  15
Leu Cys Ile His Glu Arg Tyr His Ser Val Leu Gln Pro Leu Asp Ile
                20                  25                  30
Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala
            35                  40                  45
Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu
        50                  55                  60
Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu Ser His Val His
65                  70                  75                  80
Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile Ser Gly Tyr Asn
                85                  90                  95
Leu Phe His Glu Ala Ile Pro Asp Pro Ser Trp Lys Asp Thr Val Leu
                100                 105                 110
Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu Asp Met Phe Pro Asp Tyr
            115                 120                 125
Gly Tyr Gly Trp Phe His Thr Ser Leu Ile Leu Glu Gly Lys Asn Tyr
        130                 135                 140
Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu Arg Gly Val Lys Phe Phe
145                 150                 155                 160
Gln Arg Lys Val Glu Ser Phe Glu Glu Val Ala Arg Glu Gly Ala Asp
                165                 170                 175
Val Ile Val Asn Cys·Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp
                180                 185                 190
Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile Met Lys Asp Pro Asp Ser
            195                 200                 205
Tyr Ser Trp Arg His Leu Pro Val Gly Lys Leu Glu
    210                 215                 220
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<210> 9
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<213> Homo sapiens

<400> 9
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Met Arg Val Val Val Ile Gly Ala Gly Val Ile Gly Leu Ser Thr Ala
1               5                   10                  15
Leu Cys Ile His Glu Arg Tyr His Ser Val Leu Gln Pro Leu Asp Ile
                20                  25                  30
Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala
            35                  40                  45
Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu
        50                  55                  60
Ala Thr Leu Pro Gly Arg Thr Gln Phe Trp Asp Phe Gly Ser
65                  70                  75
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<212> PRT
<213> Homo sapiens

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Met Arg Val Val Ile Gly Ala Gly Val Ile Gly Leu Ser Thr Ala
1   5   10   15
Leu Cys Ile His Glu Arg Tyr His Ser Val Leu Gln Pro Leu Asp Ile
                20   25   30
Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala
        35   40   45
Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu
    50   55   60
Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu Ser His Val His
65   70   75   80
Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile Ser Gly Tyr Asn
                85   90   95
Leu Phe His Glu Ala Ile Pro Val Ala Arg Glu Gly Ala Asp Val Ile
                100   105   110
Val Asn Cys Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp Pro Leu
            115   120   125
Leu Gln Pro Gly Arg Gly Gln Ile Met Lys Val Asp Ala Pro Trp Met
        130   135   140
Lys His Phe Ile Leu Thr His Asp Pro Glu Arg Gly Ile Tyr Asn Ser
145   150   155   160
Pro Tyr Ile Ile Pro Gly Thr Gln Thr Val Thr Leu Gly Gly Ile Phe
                165   170   175
Gln Leu Gly Asn Trp Ser Glu Leu Asn Asn Ile Gln Asp His Asn Thr
            180   185   190
Ile Trp Glu Gly Cys Cys Arg Leu Glu Pro Thr Leu Lys Asn Ala Arg
        195   200   205
Ile Ile Gly Glu Arg Thr Gly Phe Arg Pro Val Arg Pro Gln Ile Arg
    210   215   220
Leu Glu Arg Glu Gln Leu Arg Thr Gly Pro Ser Asn Thr Glu Val Ile
225   230   235   240
His Asn Tyr Gly His Gly Gly Tyr Gly Leu Thr Ile His Trp Gly Cys
                245   250   255
Ala Leu Glu Ala Ala Lys Leu Phe Gly Arg Ile Leu Glu Glu Lys Lys
            260   265   270
Leu Ser Arg Met Pro Pro Ser His Leu
        275   280

<210> 11
<211> 456
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 152
<223> 99-16105-152 : polymorphic base A or G

<220>
<221> misc_binding
<222> 140..164
<223> 99-16105-152.probe

<220>

<221> primer_bind
<222> 133..151
<223> 99-16105-152.mis

<220>
<221> primer_bind
<222> 153..171
<223> 99-16105-152.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-16105.pu

<220>
<221> primer_bind
<222> 437..456
<223> 99-16105.rp complement

<400> 11

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cgctttgttg tattctttgt tatttatcca ttttgccaaa ttatctgcaa gtagaaatat    60
cgaaataaga agctctttag caatttactt tggatattgg ttttcttttg aaggacagtt   120
attaaaatag cttgtaggat tactcatttt crtttttctt cttttaaat ataaagcaat   180
gtcatcactt ttttcccctgt attatatttc tcctcaataa ttgatatgct acattaaagg   240
aacacaaaat ggtcttaatt atgcaataat gatcaaggca aagagtgttt cctgggaact   300
aatggttgcc tgagaggagg tgatggcttg aggtccagct ggttattaag ccgcaggaaa   360
tgctgcaggc caagatttgt attatttctc tgagatgaaa atgaacccaa aaaaaggcaa   420
aatgggtttt tctccactaa tgggtaaaat gaactc                             456
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<210> 12
<211> 463
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 215
<223> 99-5919-215 : polymorphic base A or G

<220>
<221> misc_binding
<222> 203..227
<223> 99-5919-215.probe

<220>
<221> primer_bind
<222> 196..214
<223> 99-5919-215.mis

<220>
<221> primer_bind
<222> 216..234
<223> 99-5919-215.mis complement

<220>
<221> primer_bind
<222> 11..29
<223> 99-5919.pu

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<220>
<221> primer_bind
<222> 445..465
<223> 99-5919.rp complement

<400> 12
tttctcttga ctacagcaat gcagatttca attctgccat tgaattccca gacatattcg      60
tcatccccat tttcatcccc caccaccctg ccattttctt cgtgttaact tgtttcctg      120
actcacagaa atcacctttt cctgtataca tttttaggat gtcagacttt attctaatga     180
tttctcctag ttgcccccca aaattgtatt ctacrgtgtg attttaaagc tgaattttca     240
agatgatatt tcatatctat attttcacaa gcttttcttc tatgaatgtt attgtcagct     300
gtcagggtgt gagatggtac ttgatactac attctttcca agctgttgcc tgaatcggtt     360
taagacaaag tcattactag gctgtaaact gttgctctgc aaaattgagc agcacgtatt     420
taaccactca tacttcttag ctctccaaca ctttgagtcr ata                       463


<210> 13
<211> 742
<212> DNA
<213> Homo sapiens


<220>
<221> 5'UTR
<222> 1..46


<220>
<221> CDS
<222> 47..508


<220>
<221> 3'UTR
<222> 509..742


<220>
<221> polyA_signal
<222> 718..723


<220>
<221> allele
<222> 21
<223> 8-135-112   : polymorphic base C or T


<220>
<221> allele
<222> 75
<223> 8-135-166   : polymorphic base A or C


<220>
<221> allele
<222> 135
<223> 99-16038-118   : polymorphic base A or G


<220>
<221> allele
<222> 194
<223> 8-137-152   : polymorphic base G or T


<220>
<221> allele
<222> 224
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<223> 8-137-182   : polymorphic base A or G

<220>
<221> allele
<222> 390
<223> 8-130-220   : polymorphic base A or C

<220>
<221> allele
<222> 406
<223> 8-130-236   : polymorphic base A or G

<220>
<221> allele
<222> 578
<223> 8-131-199   : polymorphic base A or C

<220>
<221> allele
<222> 641
<223> 8-132-97   : polymorphic base C or T

<220>
<221> allele
<222> 708
<223> 8-132-164   : polymorphic base C or T

<220>
<221> allele
<222> 723
<223> 8-132-179   : polymorphic base A or T

<400> 13

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tcatctctgc ttcacaatgc ygatgattta gctgggagga cccaaa atg ctg gaa        55
                                                  Met Leu Glu
                                                   1

aag ctg atg ggt gct gat tmt ctc cag ctt ttc aga tcc aga tat aca       103
Lys Leu Met Gly Ala Asp Xaa Leu Gln Leu Phe Arg Ser Arg Tyr Thr
    5                   10                  15

ttg ggt aaa atc tac ttc ata ggt ttt caa arg agc att ctt ctg agc       151
Leu Gly Lys Ile Tyr Phe Ile Gly Phe Gln Xaa Ser Ile Leu Leu Ser
20                  25                  30                      35

aaa tct gaa aac tct cta aac tct att gca aag gag aca gaa kaa gga       199
Lys Ser Glu Asn Ser Leu Asn Ser Ile Ala Lys Glu Thr Glu Xaa Gly
                40                  45                  50

aga gag acg gta aca agg aaa gaa rga tgg aag aga agg cat gag gac       247
Arg Glu Thr Val Thr Arg Lys Glu Xaa Trp Lys Arg Arg His Glu Asp
            55                  60                  65

ggc tat ttg gaa atg gca cag agg cat tta cag aga tca tta tgt cct       295
Gly Tyr Leu Glu Met Ala Gln Arg His Leu Gln Arg Ser Leu Cys Pro
        70                  75                  80

tgg gtc tct tac ctt cct cag ccc tat gca gag ctt gaa gaa gta agc       343
Trp Val Ser Tyr Leu Pro Gln Pro Tyr Ala Glu Leu Glu Glu Val Ser
        85                  90                  95

agc cat gtt gga aaa gtc ttc atg gca aga aac tat gag ttc ctt gmc       391
Ser His Val Gly Lys Val Phe Met Ala Arg Asn Tyr Glu Phe Leu Xaa
100                 105                 110                     115

tat gag gcc tct aar gac cgc agg cag cct cta gaa cga atg tgg acc       439
Tyr Glu Ala Ser Lys Asp Arg Arg Gln Pro Leu Glu Arg Met Trp Thr
```

42

```
                  120                    125                    130
tgc aac tac aac cag caa aaa gac cag tca tgc aac cac aag gaa ata      487
Cys Asn Tyr Asn Gln Gln Lys Asp Gln Ser Cys Asn His Lys Glu Ile
                   135                    140                    145
act tct acc aaa gct gaa tga gtttggaagc agattcttcc cagccaatcc        538
Thr Ser Thr Lys Ala Glu  *
            150
ttctgatgac aatgtagtct ggccaacatc ttcactggam tctgacggac tctgtgtctg   598
ggacccagct gataacacgt ggtgatggga ttgtatttgc aaytctctgg tcagtaagtg   658
ataaaatgcc atttctatgc acccacctgg cctgtgtgca tgggagaaty tctctttta    718
ttaawtgtgc ttcaagtttt aaca                                          742


<210> 14
<211> 153
<212> PRT
<213> Homo sapiens

<400> 14
Met Leu Glu Lys Leu Met Gly Ala Asp Xaa Leu Gln Leu Phe Arg Ser
1               5                   10                  15
Arg Tyr Thr Leu Gly Lys Ile Tyr Phe Ile Gly Phe Gln Xaa Ser Ile
            20                  25                  30
Leu Leu Ser Lys Ser Glu Asn Ser Leu Asn Ser Ile Ala Lys Glu Thr
        35                  40                  45
Glu Xaa Gly Arg Glu Thr Val Thr Arg Lys Glu Xaa Trp Lys Arg Arg
    50                  55                  60
His Glu Asp Gly Tyr Leu Glu Met Ala Gln His Leu Gln Arg Ser
65                  70                  75                  80
Leu Cys Pro Trp Val Ser Tyr Leu Pro Gln Pro Tyr Ala Glu Leu Glu
                85                  90                  95
Glu Val Ser Ser His Val Gly Lys Val Phe Met Ala Arg Asn Tyr Glu
            100                 105                 110
Phe Leu Xaa Tyr Glu Ala Ser Lys Asp Arg Arg Gln Pro Leu Glu Arg
        115                 120                 125
Met Trp Thr Cys Asn Tyr Asn Gln Gln Lys Asp Gln Ser Cys Asn His
    130                 135                 140
Lys Glu Ile Thr Ser Thr Lys Ala Glu
145                 150


<210> 15
<211> 476
<212> DNA
<213> Homo sapiens

<400> 15
cat gag gac ggc tat ttg gaa atg gca cag agg cat tta cag aga tca     48
His Glu Asp Gly Tyr Leu Glu Met Ala Gln Arg His Leu Gln Arg Ser
1               5                   10                  15
tta tgt cct tgg gtc tct tac ctt cct cag ccc tat gca gag ctt gaa     96
Leu Cys Pro Trp Val Ser Tyr Leu Pro Gln Pro Tyr Ala Glu Leu Glu
            20                  25                  30
gaa gta agc agc cat gtt gga aaa gtc ttc atg gca aga aac tat gag    144
Glu Val Ser Ser His Val Gly Lys Val Phe Met Ala Arg Asn Tyr Glu
        35                  40                  45
ttc ctt gcc tat gag gcc tct aag gac cgc agg cag cct cta gaa cga    192
Phe Leu Ala Tyr Glu Ala Ser Lys Asp Arg Arg Gln Pro Leu Glu Arg
        50                  55                  60
atg tgg acc tgc aac tac aac cag caa aaa gac cag tca tgc aac cac    240
Met Trp Thr Cys Asn Tyr Asn Gln Gln Lys Asp Gln Ser Cys Asn His
```

43

```
             65                    70                    75                    80
aag gaa ata act tct acc aaa gct gaa tga gtttggaagc agattcttcc          290
Lys Glu Ile Thr Ser Thr Lys Ala Glu  *
                        85                    90
cagccaatcc ttctgatgac aatgtagtcc ggccaacatc ttcactggac tctgacggac        350
tctgtgtctg ggacccagct gataacacgt ggtgatggga ttgtatttgc aactctctgg        410
tcagtaagtg ataaaatgcc atttctatgc acccacctgg cctgtgtgac tgggagaatc        470
tctctt                                                                   476


<210> 16
<211> 89
<212> PRT
<213> Homo sapiens


<400> 16
His Glu Asp Gly Tyr Leu Glu Met Ala Gln Arg His Leu Gln Arg Ser
1               5                   10                  15
Leu Cys Pro Trp Val Ser Tyr Leu Pro Gln Pro Tyr Ala Glu Leu Glu
                20                  25                  30
Glu Val Ser Ser His Val Gly Lys Val Phe Met Ala Arg Asn Tyr Glu
            35                  40                  45
Phe Leu Ala Tyr Glu Ala Ser Lys Asp Arg Arg Gln Pro Leu Glu Arg
        50                  55                  60
Met Trp Thr Cys Asn Tyr Asn Gln Gln Lys Asp Gln Ser Cys Asn His
65                  70                  75                  80
Lys Glu Ile Thr Ser Thr Lys Ala Glu
                    85


<210> 17
<211> 1633
<212> DNA
<213> Homo sapiens


<400> 17
ttggggtcca ttgcaacccg aggcgagact agagttccca agcgagaagg gaagaggcag        60
tgggtgcacg tggaagggcag acagagggct ggaaacaaga cgctccagaa tcaggagctt       120
cccctcagga aatagcatcc tgtgtgtccccg cactgcagtt gtctggtgtc tccagcagtt      180
tggtacttcc ggctgctgca atg cgt gtg gtg gtg gtg att gga gca gga gtc atc     233
                        Met Arg Val Val Val Val Ile Gly Ala Gly Val Ile
                        1                   5                   10
ggg ctg tcc acc gcc ctc tgc atc cat gag cgc tac cac tca gtc ctg          281
Gly Leu Ser Thr Ala Leu Cys Ile His Glu Arg Tyr His Ser Val Leu
            15                  20                  25
cag cca ctg cac ata aag gtc tac gcg gac cgc ttc acc cca ctc acc          329
Gln Pro Leu His Ile Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr
        30                  35                  40
acc acc gac gtg gct gcc ggc ctc tgg cag ccc tac ctt tct gac ccc          377
Thr Thr Asp Val Ala Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro
    45                  50                  55
aac aac cca cag gag gcg gac tgg agc caa cag acc ttt gac tat ctc          425
Asn Asn Pro Gln Glu Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu
60                  65                  70                  75
ctg agc cat gtc cat tct ccc aac gct gaa aac ctg ggc ctg ttc cta          473
Leu Ser His Val His Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu
                80                  85                  90
atc tcg ggc tac aac ctc ttc cat gaa gcc att ccg gac cct tcc tgg          521
Ile Ser Gly Tyr Asn Leu Phe His Glu Ala Ile Pro Asp Pro Ser Trp
                95                  100                 105
aag gac aca gtt ctg gga ttt cgg aag cgt acc ccc aga gag ctg gat          569
```

                                    44

```
Lys Asp Thr Val Leu Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu Asp
        110                 115                 120
atg ttc cca gat tac ggc tat ggc tgg ttc cac aca agc cta att ctg      617
Met Phe Pro Asp Tyr Gly Tyr Gly Trp Phe His Thr Ser Leu Ile Leu
    125                 130                 135
gag gga aag aac tat cta cag tgg ctg act gaa agg tta act gag agg      665
Glu Gly Lys Asn Tyr Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu Arg
140                 145                 150                 155
gga gtg aag ttc ttc cag cgg aaa gtg gag tct ttt gag gag gtg gca      713
Gly Val Lys Phe Phe Gln Arg Lys Val Glu Ser Phe Glu Glu Val Ala
                160                 165                 170
aga gaa ggc gca gac gtg att gtc aac tgc act ggg gta tgg gct ggg      761
Arg Glu Gly Ala Asp Val Ile Val Asn Cys Thr Gly Val Trp Ala Gly
            175                 180                 185
gcg cta caa cga gac ccc ctg ctg cag cca ggc cgg ggg cag atc atg      809
Ala Leu Gln Arg Asp Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile Met
        190                 195                 200
aag gtg gac gcc cct tgg atg aag cac ttc att ctc acc cat gac cca      857
Lys Val Asp Ala Pro Trp Met Lys His Phe Ile Leu Thr His Asp Pro
    205                 210                 215
gag aga ggc atc tac aat tcc ccg tac atc atc cca ggg acc cag aca      905
Glu Arg Gly Ile Tyr Asn Ser Pro Tyr Ile Ile Pro Gly Thr Gln Thr
220                 225                 230                 235
gtt act ctt gga ggc atc ttc cag ttg gga aac tgg agt gaa cta aac      953
Val Thr Leu Gly Gly Ile Phe Gln Leu Gly Asn Trp Ser Glu Leu Asn
                240                 245                 250
aat atc cag gac cac aac acc att tgg gaa ggc tgc tgc aga ctg gag     1001
Asn Ile Gln Asp His Asn Thr Ile Trp Glu Gly Cys Cys Arg Leu Glu
            255                 260                 265
ccc aca ctg aag aat gca aga att att ggt gaa gca act ggc ttc cgg     1049
Pro Thr Leu Lys Asn Ala Arg Ile Ile Gly Glu Ala Thr Gly Phe Arg
        270                 275                 280
cca gta cgc ccc cag att cgg cta gaa aga gaa cag ctt cgc act gga     1097
Pro Val Arg Pro Gln Ile Arg Leu Glu Arg Glu Gln Leu Arg Thr Gly
    285                 290                 295
cct tca aac aca gag gtc atc cac aac tat ggc cat gga ggc tac ggg     1145
Pro Ser Asn Thr Glu Val Ile His Asn Tyr Gly His Gly Gly Tyr Gly
300                 305                 310                 315
ctc acc atc cac tgg gga tgt gcc ctg gag gca gcc aag ctc ttt ggg     1193
Leu Thr Ile His Trp Gly Cys Ala Leu Glu Ala Ala Lys Leu Phe Gly
                320                 325                 330
aga atc ctg gaa gaa aag aaa ttg tcc aga atg cca cca tcc cac ctc     1241
Arg Ile Leu Glu Glu Lys Lys Leu Ser Arg Met Pro Pro Ser His Leu
            335                 340                 345
tga agactccagt gactgctgcc tccccccaca agaactccct tctcccctca          1294
  *
gccaatgaat caatgtgctc cttcataagc cattgcttct ccctcacttc tttcctcaaa   1354
gaagcatgag gtgagagaaa gccacraagt cagtgcctgg agaaggggttc agcccaacat   1414
gggggcccctc tcatcactga aatccctcta ccttctctgg gtctggcatt ataaagaaca   1474
gctgaggctg tcattccatg agtcttcaga agaaaaggaca gctcagaaag tcaaagaggc    1534
caactgccca gagccacaga aaatggagga taattgaggc taagtaacct gattacaagt    1594
tgtactaaca tattaaaggt tctgaaaagt cctgcaaaa                           1633

<210> 18
<211> 347
<212> PRT
<213> Homo sapiens

<400> 18
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Met Arg Val Val Val Ile Gly Ala Gly Val Ile Gly Leu Ser Thr Ala
1               5                   10                  15
Leu Cys Ile His Glu Arg Tyr His Ser Val Leu Gln Pro Leu Asp Ile
            20                  25                  30
Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala
        35                  40                  45
Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu
    50                  55                  60
Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu Ser His Val His
65                  70                  75                  80
Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile Ser Gly Tyr Asn
                85                  90                  95
Leu Phe His Glu Ala Ile Pro Asp Pro Ser Trp Lys Asp Thr Val Leu
            100                 105                 110
Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu Asp Met Phe Pro Asp Tyr
        115                 120                 125
Gly Tyr Gly Trp Phe His Thr Ser Leu Ile Leu Glu Gly Lys Asn Tyr
    130                 135                 140
Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu Arg Gly Val Lys Phe Phe
145                 150                 155                 160
Gln Arg Lys Val Glu Ser Phe Glu Glu Val Ala Arg Glu Gly Ala Asp
                165                 170                 175
Val Ile Val Asn Cys Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp
            180                 185                 190
Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile Met Lys Val Asp Ala Pro
        195                 200                 205
Trp Met Lys His Phe Ile Leu Thr His Asp Pro Glu Arg Gly Ile Tyr
    210                 215                 220
Asn Ser Pro Tyr Ile Ile Pro Gly Thr Gln Thr Val Thr Leu Gly Gly
225                 230                 235                 240
Ile Phe Gln Leu Gly Asn Trp Ser Glu Leu Asn Asn Ile Gln Asp His
                245                 250                 255
Asn Thr Ile Trp Glu Gly Cys Cys Arg Leu Glu Pro Thr Leu Lys Asn
            260                 265                 270
Ala Arg Ile Ile Gly Glu Ala Thr Gly Phe Arg Pro Val Arg Pro Gln
        275                 280                 285
Ile Arg Leu Glu Arg Glu Gln Leu Arg Thr Gly Pro Ser Asn Thr Glu
    290                 295                 300
Val Ile His Asn Tyr Gly His Gly Gly Tyr Gly Leu Thr Ile His Trp
305                 310                 315                 320
Gly Cys Ala Leu Glu Ala Ala Lys Leu Phe Gly Arg Ile Leu Glu Glu
                325                 330                 335
Lys Lys Leu Ser Arg Met Pro Pro Ser His Leu
            340                 345
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<210> 19
<211> 1200
<212> DNA
<213> Homo sapiens

<400> 19
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atg gac aca gca cgg att gca gtt gtc ggg gca ggt gtg gtg ggg ctc    48
Met Asp Thr Ala Arg Ile Ala Val Val Gly Ala Gly Val Val Gly Leu
1               5                   10                  15

tcc acg gct gtg tgc atc tcc aaa ctg gtg ccc cga tgc tcc gtt acc    96
Ser Thr Ala Val Cys Ile Ser Lys Leu Val Pro Arg Cys Ser Val Thr
            20                  25                  30

atc att tca gac aag ttt act cca gat acc acc agt gat gtg gca gcc   144
Ile Ile Ser Asp Lys Phe Thr Pro Asp Thr Thr Ser Asp Val Ala Ala
```

```
          35                        40                        45
gga atg ctt att cct cac act tat cca gat aca ccc att cac acg cag   192
Gly Met Leu Ile Pro His Thr Tyr Pro Asp Thr Pro Ile His Thr Gln
     50                        55                        60
aag cag tgg ttc aga gaa acc ttt aat cac ctc ttt gca att gcc aat   240
Lys Gln Trp Phe Arg Glu Thr Phe Asn His Leu Phe Ala Ile Ala Asn
65                        70                        75                        80
tct gca gaa gct gga gat gct ggt gtt cat ttg gta tca ggt tgg cag   288
Ser Ala Glu Ala Gly Asp Ala Gly Val His Leu Val Ser Gly Trp Gln
                    85                        90                        95
ata ttt cag agc act ccg act gaa gaa gtg cca ttc tgg gct gac gtg   336
Ile Phe Gln Ser Thr Pro Thr Glu Glu Val Pro Phe Trp Ala Asp Val
               100                       105                       110
gtt ctg gga ttt cga aag atg act gag gct gag ctg aag aaa ttc ccc   384
Val Leu Gly Phe Arg Lys Met Thr Glu Ala Glu Leu Lys Lys Phe Pro
               115                       120                       125
cag tat gtg ttt ggt cag gct ttt aca acc ctg aaa tgt gaa tgc cct   432
Gln Tyr Val Phe Gly Gln Ala Phe Thr Thr Leu Lys Cys Glu Cys Pro
          130                       135                       140
gcc tac ctc ccg tgg ttg gag aaa agg ata aag gga agt gga ggc tgg   480
Ala Tyr Leu Pro Trp Leu Glu Lys Arg Ile Lys Gly Ser Gly Gly Trp
145                       150                       155                       160
aca ctc act cgg aga ata gaa gac ctg tgg gaa ctt cat ccg tcc ttt   528
Thr Leu Thr Arg Arg Ile Glu Asp Leu Trp Glu Leu His Pro Ser Phe
                    165                       170                       175
gac atc gtg gtc aac tgt tca ggc ctt gga agc aga cag ctt gca gga   576
Asp Ile Val Val Asn Cys Ser Gly Leu Gly Ser Arg Gln Leu Ala Gly
               180                       185                       190
gac tca aag att ctc cct gta agg ggc caa gtc ctc caa gtt cag gca   624
Asp Ser Lys Ile Leu Pro Val Arg Gly Gln Val Leu Gln Val Gln Ala
               195                       200                       205
ccc tgg gtg gag cat ttt atc cga gat ggc agt ggg ctg aca tat att   672
Pro Trp Val Glu His Phe Ile Arg Asp Gly Ser Gly Leu Thr Tyr Ile
          210                       215                       220
tat cct ggt aca tcc cat gta acc cta ggt gga act agg caa aaa ggg   720
Tyr Pro Gly Thr Ser His Val Thr Leu Gly Gly Thr Arg Gln Lys Gly
225                       230                       235                       240
gac tgg aat ctg tcc ccg gat gca gaa aat agc aga gag att ctt tcc   768
Asp Trp Asn Leu Ser Pro Asp Ala Glu Asn Ser Arg Glu Ile Leu Ser
                    245                       250                       255
cga tgc tgt gct ctg gag ccc tcc ctc cac gga gcc tgc aac atc agg   816
Arg Cys Cys Ala Leu Glu Pro Ser Leu His Gly Ala Cys Asn Ile Arg
               260                       265                       270
gag aag gtg ggc ttg agg ccc tac agg cca ggc gtg cga ctg cag aca   864
Glu Lys Val Gly Leu Arg Pro Tyr Arg Pro Gly Val Arg Leu Gln Thr
               275                       280                       285
gag ctc ctt gcg cga gat gga cag agg ctg cct gta gtc cac cac tat   912
Glu Leu Leu Ala Arg Asp Gly Gln Arg Leu Pro Val Val His His Tyr
          290                       295                       300
ggc cat ggg agt ggg ggc atc tca gtg cac tgg ggc act gct ctg gag   960
Gly His Gly Ser Gly Gly Ile Ser Val His Trp Gly Thr Ala Leu Glu
305                       310                       315                       320
gcc gcc agg ctg gtg agc gag tgt gtc cat gcc ctc agg acc ccc att   1008
Ala Ala Arg Leu Val Ser Glu Cys Val His Ala Leu Arg Thr Pro Ile
                    325                       330                       335
ccc aag tca aac ctg tag atgacataaa atgacagcaa agagactgag           1056
Pro Lys Ser Asn Leu  *
               340

agactgttga tcaaagcaca gaacaggttc aaataacttt tccactgcat gaaagtttaa   1116
```

47

```
ttagacattt ctttgttttc aacattagaa gtggtgtaac atgtaagctg agcacggtag    1176
catgcctata gtcccagcta cttg                                           1200


<210> 20
<211> 2056
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 1025
<223> n=a, g, c or t

<400> 20
atg gac aca gca cgg att gca gtt gtc ggg gca ggt gtg gtg ggg ctc      48
Met Asp Thr Ala Arg Ile Ala Val Val Gly Ala Gly Val Val Gly Leu
1               5                   10                  15
tcc acg gct gtg tgc atc tcc aaa ctg gtg ccc cga tgc tcc gtt acc      96
Ser Thr Ala Val Cys Ile Ser Lys Leu Val Pro Arg Cys Ser Val Thr
                20                  25                  30
atc att tca gac aag ttt act cca gat acc acc agt gat gtg gca gcc     144
Ile Ile Ser Asp Lys Phe Thr Pro Asp Thr Thr Ser Asp Val Ala Ala
            35                  40                  45
gga atg ctt att cct cac act tat cca gat aca ccc att cac acg cag     192
Gly Met Leu Ile Pro His Thr Tyr Pro Asp Thr Pro Ile His Thr Gln
        50                  55                  60
aag cag tgg ttc aga gaa acc ttt aat cac ctc ttt gca att gcc aat     240
Lys Gln Trp Phe Arg Glu Thr Phe Asn His Leu Phe Ala Ile Ala Asn
65                  70                  75                  80
tct gca gaa gct gga gat gct ggt gtt cat ttg gta tca ggg ata aag     288
Ser Ala Glu Ala Gly Asp Ala Gly Val His Leu Val Ser Gly Ile Lys
                85                  90                  95
gga agt gga ggc tgg aca ctc act cgg cga ata gaa gac ctg tgg gaa     336
Gly Ser Gly Gly Trp Thr Leu Thr Arg Arg Ile Glu Asp Leu Trp Glu
            100                 105                 110
ctt cat ccg tcc ttt gac atc gtg gtc aac tgt tca ggc ctt gga agc     384
Leu His Pro Ser Phe Asp Ile Val Val Asn Cys Ser Gly Leu Gly Ser
        115                 120                 125
aga cag ctt gca gga gac tca aag att ttc cct gta agg ggc caa gtc     432
Arg Gln Leu Ala Gly Asp Ser Lys Ile Phe Pro Val Arg Gly Gln Val
    130                 135                 140
ctc caa gtt cag gct ccc tgg gtg gag cat ttt atc cga gat ggc agt     480
Leu Gln Val Gln Ala Pro Trp Val Glu His Phe Ile Arg Asp Gly Ser
145                 150                 155                 160
ggg ctg aca tat att tat cct ggt aca tcc cat gta acc cta ggt gga     528
Gly Leu Thr Tyr Ile Tyr Pro Gly Thr Ser His Val Thr Leu Gly Gly
                165                 170                 175
act agg caa aaa ggg gac tgg aat ctg tcc ccg gat gca gaa aat agc     576
Thr Arg Gln Lys Gly Asp Trp Asn Leu Ser Pro Asp Ala Glu Asn Ser
            180                 185                 190
aga gag att ctt tcc cga tgc tgt cgc gca ctc gag ccc tcc ctc cac gga 624
Arg Glu Ile Leu Ser Arg Cys Cys Arg Ala Leu Glu Pro Ser Leu His Gly
    195                 200                 205
gcc tgc aac atc agg gag aag gtg ggc ttg agg ccc tac agg cca ggc     672
Ala Cys Asn Ile Arg Glu Lys Val Gly Leu Arg Pro Tyr Arg Pro Gly
    210                 215                 220
gtg cga ctg cag aca gag ctc ctt gcg cga gat gga cag agg ctg cct     720
Val Arg Leu Gln Thr Glu Leu Leu Ala Arg Asp Gly Gln Arg Leu Pro
225                 230                 235                 240
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48

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gta gtc cac cac tat ggc cat ggg agt ggg ggc atc tca gtg cac tgg        768
Val Val His His Tyr Gly His Gly Ser Gly Gly Ile Ser Val His Trp
                  245                 250                 255
ggc act gct ctg gag gcc gcc agg ctg gtg agc gag tgt gtc cat gcc        816
Gly Thr Ala Leu Glu Ala Ala Arg Leu Val Ser Glu Cys Val His Ala
                  260                 265                 270
ctc agg acc ccc att ccc aag tca aac ctg tag atgacataaa atgacagcaa      869
Leu Arg Thr Pro Ile Pro Lys Ser Asn Leu  *
                  275                 280
agagactgag agactgttga tcaaagcaca gaacaggttc aaataacttt tccactgcat      929
gaaagtttaa ttagacattt ctttgtttc aacattagaa gtggtgtaac atgtaagctg       989
agcacggtag catgccatta gtcccagcta cttg>nm_00 4032atggac acagcacgga     1041
ttgcagttgt cggggcaggt gtggtggggc tctccacggc tgtgtgcatc tccaaactgg     1101
tgcccgatg ctccgttacc atcatttcag acaagtttac tccagatacc accagtgatg      1161
tggcagccgg aatgcttatt cctcacactt atccagatac acccattcac acgcagaagc     1221
agtggttcag agaaaccttt aatcacctct ttgcaattgc caattctgca gaagctggag     1281
atgctggtgt tcatttggta tcagggataa agggaagtgg aggctggaca ctcactcggc     1341
gaatagaaga cctgtgggaa cttcatccgt cctttgacat cgtggtcaac tgttcaggcc     1401
ttggaagcag acagcttgca ggagactcaa agattttccc tgtaaggggc caagtcctcc     1461
aagttcaggc tccctgggtg gagcattta tccgagatgg cagtgggctg acatatattt      1521
atcctggtac atcccatgta accctaggtg gaactaggca aaaagggggac tggaatctgt     1581
ccccggatgc agaaaatagc agagagattc tttcccgatg ctgtgctctg gagccctccc     1641
tccacggagc ctgcaacatc agggagaagg tgggcttgca gccctacagg ccaggcgtgc     1701
gactgcagac agagctcctt gcgcgagatg gacagaggct gcctgtagtc caccactatg     1761
tgagcgagtg tgtccatgcc ctcaggaccc ccattcccaa gtcaaacctg tagatgacat     1821
aaaatgacag caaagagact gagagactgt tgatcaaagc acagaacagg ttcaaataac     1941
ttttccactg catgaaagtt taattagaca tttctttgtt ttcaacatta gaagtggtgt     2001
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<213> Homo sapiens

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Ser Thr Ala Val Cys Ile Ser Lys Leu Val Pro Arg Cys Ser Val Thr
                20                  25                  30
Ile Ile Ser Asp Lys Phe Thr Pro Asp Thr Thr Ser Asp Val Ala Ala
            35                  40                  45
Gly Met Leu Ile Pro His Thr Tyr Pro Asp Thr Pro Ile His Thr Gln
        50                  55                  60
Lys Gln Trp Phe Arg Glu Thr Phe Asn His Leu Phe Ala Ile Ala Asn
65                  70                  75                  80
Ser Ala Glu Ala Gly Asp Ala Gly Val Val Leu Val Ser Gly Trp Gln
                85                  90                  95
Ile Phe Gln Ser Thr Pro Thr Glu Glu Val Pro Phe Trp Ala Asp Val
                100                 105                 110
Val Leu Gly Phe Arg Lys Met Thr Glu Ala Glu Leu Lys Lys Phe Pro
            115                 120                 125
Gln Tyr Val Phe Gly Gln Ala Phe Thr Thr Leu Lys Cys Glu Cys Pro
        130                 135                 140
Ala Tyr Leu Pro Trp Leu Glu Lys Arg Ile Lys Gly Ser Gly Gly Trp
145                 150                 155                 160
Thr Leu Thr Arg Arg Ile Glu Asp Leu Trp Glu Leu His Pro Ser Phe
                165                 170                 175
Asp Ile Val Val Asn Cys Ser Gly Leu Gly Ser Arg Gln Leu Ala Gly
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49

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                 180                 185                 190
    Asp Ser Lys Ile Phe Pro Val Arg Gly Gln Val Leu Gln Val Gln Ala
             195                 200                 205
    Pro Trp Val Glu His Phe Ile Arg Asp Gly Ser Gly Leu Thr Tyr Ile
         210                 215                 220
    Tyr Pro Gly Thr Ser His Val Thr Leu Gly Gly Thr Arg Gln Lys Gly
    225                 230                 235                 240
    Asp Trp Asn Leu Ser Pro Asp Ala Glu Asn Ser Arg Glu Ile Leu Ser
                     245                 250                 255
    Arg Cys Cys Ala Leu Glu Pro Ser Leu His Gly Ala Cys Asn Ile Arg
             260                 265                 270
    Glu Lys Val Gly Leu Arg Pro Tyr Arg Pro Gly Val Arg Leu Gln Thr
             275                 280                 285
    Glu Leu Leu Ala Arg Asp Gly Gln Arg Leu Pro Val Val His His Tyr
         290                 295                 300
    Gly His Gly Ser Gly Gly Ile Ser Val His Trp Gly Thr Ala Leu Glu
    305                 310                 315                 320
    Ala Ala Arg Leu Val Ser Glu Cys Val His Ala Leu Arg Thr Pro Ile
                     325                 330                 335
    Pro Lys Ser Asn Leu
             340


    <210> 22
    <211> 282
    <212> PRT
    <213> Homo sapiens

    <400> 22
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    1                   5                  10                  15
    Ser Thr Ala Val Cys Ile Ser Lys Leu Val Pro Arg Cys Ser Val Thr
                     20                  25                  30
    Ile Ile Ser Asp Lys Phe Thr Pro Asp Thr Thr Ser Asp Val Ala Ala
                 35                  40                  45
    Gly Met Leu Ile Pro His Thr Tyr Pro Asp Thr Pro Ile His Thr Gln
         50                  55                  60
    Lys Gln Trp Phe Arg Glu Thr Phe Asn His Leu Phe Ala Ile Ala Asn
    65                  70                  75                  80
    Ser Ala Glu Ala Gly Asp Ala Gly Val His Leu Val Ser Gly Ile Lys
                     85                  90                  95
    Gly Ser Gly Gly Trp Thr Leu Thr Arg Arg Ile Glu Asp Leu Trp Glu
                 100                 105                 110
    Leu His Pro Ser Phe Asp Ile Val Val Asn Cys Ser Gly Leu Gly Ser
             115                 120                 125
    Arg Gln Leu Ala Gly Asp Ser Lys Ile Phe Pro Val Arg Gly Gln Val
         130                 135                 140
    Leu Gln Val Gln Ala Pro Trp Val Glu His Phe Ile Arg Asp Gly Ser
    145                 150                 155                 160
    Gly Leu Thr Tyr Ile Tyr Pro Gly Thr Ser His Val Thr Leu Gly Gly
                     165                 170                 175
    Thr Arg Gln Lys Gly Asp Trp Asn Leu Ser Pro Asp Ala Glu Asn Ser
                 180                 185                 190
    Arg Glu Ile Leu Ser Arg Cys Cys Ala Leu Glu Pro Ser Leu His Gly
             195                 200                 205
    Ala Cys Asn Ile Arg Glu Lys Val Gly Leu Arg Pro Tyr Arg Pro Gly
         210                 215                 220
    Val Arg Leu Gln Thr Glu Leu Leu Ala Arg Asp Gly Gln Arg Leu Pro
    225                 230                 235                 240
    Val Val His His Tyr Gly His Gly Ser Gly Gly Ile Ser Val His Trp
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50

```
                  245                 250                 255
Gly Thr Ala Leu Glu Ala Ala Arg Leu Val Ser Glu Cys Val His Ala
            260                 265                 270
Leu Arg Thr Pro Ile Pro Lys Ser Asn Leu
         275                 280


<210> 23
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<223> polymorphic base C or T


<210> 24
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<212> DNA
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<220>
<223> oligonucleotide 24-1457-52

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<400> 24
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<220>
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<223> polymorphic base C or T

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<222> 24
<223> polymorphic base A or G

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